

SEQUENCE LISTING

COPY

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KHOURGES, EVGENI
VOROSHILOVA, ELVIRA
GUSYATINER, MIKHAIL



<120> METHOD FOR PRODUCING L-AMINO ACID USING BACTERIA BELONGING TO THE GENUS
ESCHERICHIA

<130> 219594US0

<140> 10/073,293

<141> 2002-02-13

<150> RU 2001103865

<151> 2001-02-13

<150> RU 2001104998

<151> 2001-02-26

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<150> RU 2001117632

<151> 2001-06-28

<150> RU 2001117633

<151> 2001-06-28

<160> 16

<170> PatentIn version 3.1

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<212> DNA

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26

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ccggatccga tatagtaacg acagtg

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<221> CDS

<222> (1)..(735)

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1 5 10 15

gaa gga tgc aaa gac agt tta ccg att gtt att agt tat att ccg gtg 96
Glu Gly Cys Lys Asp Ser Leu Pro Ile Val Ile Ser Tyr Ile Pro Val
20 25 30

gcc ttt gcg ttc ggt ctg aat gcg acc cgt ctg gga ttc tct cct ctc 144
Ala Phe Ala Phe Gly Leu Asn Ala Thr Arg Leu Gly Phe Ser Pro Leu
35 40 45

gaa agc gtt ttt ttc tcc tgc atc att tat gca ggc gcg agc cag ttc 192
Glu Ser Val Phe Phe Ser Cys Ile Ile Tyr Ala Gly Ala Ser Gln Phe
50 55 60

gtc att acc gcg atg ctg gca gcc ggg agt agt ttg tgg att gct gca 240
Val Ile Thr Ala Met Leu Ala Ala Gly Ser Ser Leu Trp Ile Ala Ala
65 70 75 80

ctg acc gtc atg gca atg gat gtt cgc cat gtg ttg tat ggc ccg tca 288
Leu Thr Val Met Ala Met Asp Val Arg His Val Leu Tyr Gly Pro Ser
85 90 95

ctg cgt agc cgt att att cag cgt ctg caa aaa tcg aaa acc gcc ctg 336
Leu Arg Ser Arg Ile Ile Gln Arg Leu Gln Lys Ser Lys Thr Ala Leu
100 105 110

tgg gcg ttt ggc ctg acg gat gag gtt ttt gcc gcc gca acc gca aaa 384
Trp Ala Phe Gly Leu Thr Asp Glu Val Phe Ala Ala Ala Thr Ala Lys
115 120 125

ctg gta cgc aat aat cgc cgc tgg agc gag aac tgg atg atc ggc att 432

Leu Val Arg Asn Asn Arg Arg Trp Ser Glu Asn Trp Met Ile Gly Ile			
130	135	140	
gcc ttc agt tca tgg tca tcg tgg gta ttt ggt acg gta ata ggg gca			480
Ala Phe Ser Ser Trp Ser Trp Val Phe Gly Thr Val Ile Gly Ala			
145	150	155	160
ttc tcc ggc agc ggc ttg ctg caa ggt tat ccc gcc gtt gaa gct gca			528
Phe Ser Gly Ser Gly Leu Leu Gln Gly Tyr Pro Ala Val Glu Ala Ala			
165	170	175	
tta ggt ttt atg ctt ccg gca ctc ttt atg agt ttc ctg ctc gcc tct			576
Leu Gly Phe Met Leu Pro Ala Leu Phe Met Ser Phe Leu Leu Ala Ser			
180	185	190	
ttc cag cgc aaa caa tct ctt tgc gtt acc gca gcg tta gtt ggt gcc			624
Phe Gln Arg Lys Gln Ser Leu Cys Val Thr Ala Ala Leu Val Gly Ala			
195	200	205	
ctt gca ggc gta acg cta ttt tct att ccc gtc gcc att ctg gca ggc			672
Leu Ala Gly Val Thr Leu Phe Ser Ile Pro Val Ala Ile Leu Ala Gly			
210	215	220	
att gtc tgt ggc tgc ctc act gcg tta atc cag gca ttc tgg caa gga			720
Ile Val Cys Gly Cys Leu Thr Ala Leu Ile Gln Ala Phe Trp Gln Gly			
225	230	235	240
gcg ccc gat gag cta tga			738
Ala Pro Asp Glu Leu			
245			

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<211> 245

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<213> Escherichia coli

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Glu Gly Cys Lys Asp Ser Leu Pro Ile Val Ile Ser Tyr Ile Pro Val			
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Ala Phe Ala Phe Gly Leu Asn Ala Thr Arg Leu Gly Phe Ser Pro Leu
35 40 45

Glu Ser Val Phe Phe Ser Cys Ile Ile Tyr Ala Gly Ala Ser Gln Phe
50 55 60

Val Ile Thr Ala Met Leu Ala Ala Gly Ser Ser Leu Trp Ile Ala Ala
65 70 75 80

Leu Thr Val Met Ala Met Asp Val Arg His Val Leu Tyr Gly Pro Ser
85 90 95

Leu Arg Ser Arg Ile Ile Gln Arg Leu Gln Lys Ser Lys Thr Ala Leu
100 105 110

Trp Ala Phe Gly Leu Thr Asp Glu Val Phe Ala Ala Ala Thr Ala Lys
115 120 125

Leu Val Arg Asn Asn Arg Arg Trp Ser Glu Asn Trp Met Ile Gly Ile
130 135 140

Ala Phe Ser Ser Trp Ser Ser Trp Val Phe Gly Thr Val Ile Gly Ala
145 150 155 160

Phe Ser Gly Ser Gly Leu Leu Gln Gly Tyr Pro Ala Val Glu Ala Ala
165 170 175

Leu Gly Phe Met Leu Pro Ala Leu Phe Met Ser Phe Leu Leu Ala Ser
180 185 190

Phe Gln Arg Lys Gln Ser Leu Cys Val Thr Ala Ala Leu Val Gly Ala
195 200 205

Leu Ala Gly Val Thr Leu Phe Ser Ile Pro Val Ala Ile Leu Ala Gly
210 215 220

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Ala Pro Asp Glu Leu
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tat tgc ttc cgc tat ttg ccg ctg cgc ctg cgt gtg ggt aat gcc cgc		96
Tyr Cys Phe Arg Tyr Leu Pro Leu Arg Leu Arg Val Gly Asn Ala Arg		
20 25 30		
cca acc aaa cgt ggc gcg gta ggt att ttg ctc gac acc att ggc atc		144
Pro Thr Lys Arg Gly Ala Val Gly Ile Leu Leu Asp Thr Ile Gly Ile		
35 40 45		
gcc tcg ata tgc gct ctg ctg gtt gtc tct acc gca cca gaa gtg atg		192
Ala Ser Ile Cys Ala Leu Leu Val Val Ser Thr Ala Pro Glu Val Met		
50 55 60		
cac gat aca cgc cgt ttc gtg ccc acg ctg gtc ggc ttc gcg gta ctg		240
His Asp Thr Arg Arg Phe Val Pro Thr Leu Val Gly Phe Ala Val Leu		
65 70 75 80		
ggt gcc agt ttc tat aaa aca cgc agc att atc atc cca aca ctg ctt		288
Gly Ala Ser Phe Tyr Lys Thr Arg Ser Ile Ile Ile Pro Thr Leu Leu		
85 90 95		
agt gcg ctg gcc tat ggg ctc gcc tgg aaa gtg atg gcg att ata taa		336
Ser Ala Leu Ala Tyr Gly Leu Ala Trp Lys Val Met Ala Ile Ile		
100 105 110		

<210> 6

<211> 111

<212> PRT

<213> Escherichia coli

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20 25 30

Pro Thr Lys Arg Gly Ala Val Gly Ile Leu Leu Asp Thr Ile Gly Ile
35 40 45

Ala Ser Ile Cys Ala Leu Leu Val Val Ser Thr Ala Pro Glu Val Met
50 55 60

His Asp Thr Arg Arg Phe Val Pro Thr Leu Val Gly Phe Ala Val Leu
65 70 75 80

Gly Ala Ser Phe Tyr Lys Thr Arg Ser Ile Ile Ile Pro Thr Leu Leu
85 90 95

Ser Ala Leu Ala Tyr Gly Leu Ala Trp Lys Val Met Ala Ile Ile
100 105 110

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<400> 8
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ggtagata tggctaacat tatccggc 28

<210> 10

<211> 28

<212> DNA

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<400> 10
ccggatccaa acggagcatg gcagctcc 28

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1 5 10 15

ggg tta ttt gcg ctg gtc aac ccg gta ggg att att ccc gtc ttt atc 96
Gly Leu Phe Ala Leu Val Asn Pro Val Gly Ile Ile Pro Val Phe Ile
20 25 30

agc atg acc agt tat cag aca gcg gca gcg cga aac aaa act aac ctt 144
Ser Met Thr Ser Tyr Gln Thr Ala Ala Ala Arg Asn Lys Thr Asn Leu
35 40 45

aca gcc aac ctg tct gtg gcc att atc ttg tgg atc tcg ctt ttt ctc 192
Thr Ala Asn Leu Ser Val Ala Ile Ile Leu Trp Ile Ser Leu Phe Leu
50 55 60

ggc gac acg att cta caa ctt ttt ggt ata tca att gat tcg ttc cgt 240
Gly Asp Thr Ile Leu Gln Leu Phe Gly Ile Ser Ile Asp Ser Phe Arg
65 70 75 80

atc gcc ggg ggt atc ctg gtg gtg aca ata gcg atg tcg atg atc agc 288
Ile Ala Gly Gly Ile Leu Val Val Thr Ile Ala Met Ser Met Ile Ser
85 90 95

ggc aag ctt ggc gag gat aaa cag aac aag caa gaa aaa tca gaa acc	336
Gly Lys Leu Gly Glu Asp Lys Gln Asn Lys Gln Glu Lys Ser Glu Thr	
100 105 110	
gct gta cgt gaa agc att ggt gtg gtg cca ctg gcg ttg ccg ttg atg	384
Ala Val Arg Glu Ser Ile Gly Val Val Pro Leu Ala Leu Pro Leu Met	
115 120 125	
gct ggg cca ggg gcg atc agt tct acc atc gtc tgg ggt acg cgt tat	432
Ala Gly Pro Gly Ala Ile Ser Ser Thr Ile Val Trp Gly Thr Arg Tyr	
130 135 140	
cac agc att agc tat ctg ttt ggt ttc ttt gtg gct att gca ttg ttc	480
His Ser Ile Ser Tyr Leu Phe Gly Phe Phe Val Ala Ile Ala Leu Phe	
145 150 155 160	
gct tta tgt tgt tgg gga ttg ttc cgc atg gca ccg tgg ctg gta cgg	528
Ala Leu Cys Cys Trp Gly Leu Phe Arg Met Ala Pro Trp Leu Val Arg	
165 170 175	
gtt tta cgc cag acc ggc atc aac gtg att acg cgt att atg ggg cta	576
Val Leu Arg Gln Thr Gly Ile Asn Val Ile Thr Arg Ile Met Gly Leu	
180 185 190	
ttg ctg atg gca ttg ggg att gaa ttt atc gtt act ggt att aag ggg	624
Leu Leu Met Ala Leu Gly Ile Glu Phe Ile Val Thr Gly Ile Lys Gly	
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Gly Leu Phe Ala Leu Val Asn Pro Val Gly Ile Ile Pro Val Phe Ile	
20 25 30	

Ser Met Thr Ser Tyr Gln Thr Ala Ala Ala Arg Asn Lys Thr Asn Leu
35 40 45

Thr Ala Asn Leu Ser Val Ala Ile Ile Leu Trp Ile Ser Leu Phe Leu
50 55 60

Gly Asp Thr Ile Leu Gln Leu Phe Gly Ile Ser Ile Asp Ser Phe Arg
65 70 75 80

Ile Ala Gly Gly Ile Leu Val Val Thr Ile Ala Met Ser Met Ile Ser
85 90 95

Gly Lys Leu Gly Glu Asp Lys Gln Asn Lys Gln Glu Lys Ser Glu Thr
100 105 110

Ala Val Arg Glu Ser Ile Gly Val Val Pro Leu Ala Leu Pro Leu Met
115 120 125

Ala Gly Pro Gly Ala Ile Ser Ser Thr Ile Val Trp Gly Thr Arg Tyr
130 135 140

His Ser Ile Ser Tyr Leu Phe Gly Phe Val Ala Ile Ala Leu Phe
145 150 155 160

Ala Leu Cys Cys Trp Gly Leu Phe Arg Met Ala Pro Trp Leu Val Arg
165 170 175

Val Leu Arg Gln Thr Gly Ile Asn Val Ile Thr Arg Ile Met Gly Leu
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Leu Leu Met Ala Leu Gly Ile Glu Phe Ile Val Thr Gly Ile Lys Gly
195 200 205

Ile Phe Pro Gly Leu Leu Asn
210 215

<210> 13

<211> 28

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<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Synthetic DNA

<400> 14

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<210> 15

<211> 594

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

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1 5 10 15		
ccg ctc gga aac cta cct att ttc atg tcc gta ctg aaa cat act gaa		96
Pro Leu Gly Asn Leu Pro Ile Phe Met Ser Val Leu Lys His Thr Glu		
20 25 30		
ccg aaa aga cg ^g cg ^g gca atc atg gtg cga gag ttg ctt att gct ctc		144
Pro Lys Arg Arg Arg Ala Ile Met Val Arg Glu Leu Leu Ile Ala Leu		
35 40 45		
ctg gtg atg ctg gtg ttc ctg ttt gc ^g ggt gag aaa att ctg gca ttt		192
Leu Val Met Leu Val Phe Leu Phe Ala Gly Glu Lys Ile Leu Ala Phe		
50 55 60		
ctt agc cta cga gca gaa acc gtc tcc att tct ggc ggc atc att ctg		240
Leu Ser Leu Arg Ala Glu Thr Val Ser Ile Ser Gly Gly Ile Ile Leu		
65 70 75 80		
ttt ctg atc gcc att aaa atg att ttc ccc agc gct tca gga aat agc		288
Phe Leu Ile Ala Ile Lys Met Ile Phe Pro Ser Ala Ser Gly Asn Ser		
85 90 95		
agc ggg ctt ccg gca ggt gaa gag cca ttt atc gtg ccg ttg gca att		336
Ser Gly Leu Pro Ala Gly Glu Glu Pro Phe Ile Val Pro Leu Ala Ile		
100 105 110		
ccg tta gtc gcc ggg ccg act att ctc gcc acg ctg atg ttg ttg tct		384
Pro Leu Val Ala Gly Pro Thr Ile Leu Ala Thr Leu Met Leu Leu Ser		
115 120 125		
cat cag tac ccg aat cag atg ggg cat ctg gtg att gct ctg ctg ctg		432
His Gln Tyr Pro Asn Gln Met Gly His Leu Val Ile Ala Leu Leu Leu		
130 135 140		
gcc tgg ggc ggc acc ttt gtc atc ctg cta cag tct tcg cta ttt tta		480
Ala Trp Gly Gly Thr Phe Val Ile Leu Leu Gln Ser Ser Leu Phe Leu		
145 150 155 160		
cgt ctg ctg ggc gag aaa ggg gtg aac gca ctt gaa cgc ctg atg gga		528
Arg Leu Leu Gly Glu Lys Gly Val Asn Ala Leu Glu Arg Leu Met Gly		
165 170 175		
ttg att ctg gtg atg atg gca acc cag atg ttc ctc gac ggc att cga		576
Leu Ile Leu Val Met Met Ala Thr Gln Met Phe Leu Asp Gly Ile Arg		
180 185 190		
atg tgg atg aag ggg taa		594
Met Trp Met Lys Gly		
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<210> 16

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Pro Lys Arg Arg Arg Ala Ile Met Val Arg Glu Leu Leu Ile Ala Leu
35 40 45

Leu Val Met Leu Val Phe Leu Phe Ala Gly Glu Lys Ile Leu Ala Phe
50 55 60

Leu Ser Leu Arg Ala Glu Thr Val Ser Ile Ser Gly Gly Ile Ile Leu
65 70 75 80

Phe Leu Ile Ala Ile Lys Met Ile Phe Pro Ser Ala Ser Gly Asn Ser
85 90 95

Ser Gly Leu Pro Ala Gly Glu Glu Pro Phe Ile Val Pro Leu Ala Ile
100 105 110

Pro Leu Val Ala Gly Pro Thr Ile Leu Ala Thr Leu Met Leu Leu Ser
115 120 125

His Gln Tyr Pro Asn Gln Met Gly His Leu Val Ile Ala Leu Leu Leu
130 135 140

Ala Trp Gly Gly Thr Phe Val Ile Leu Leu Gln Ser Ser Leu Phe Leu
145 150 155 160

Arg Leu Leu Gly Glu Lys Gly Val Asn Ala Leu Glu Arg Leu Met Gly
165 170 175

Leu Ile Leu Val Met Met Ala Thr Gln Met Phe Leu Asp Gly Ile Arg
180 185 190

Met Trp Met Lys Gly
195